

#3

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,755

DATE: 01/15/2002

TIME: 17:36:26

Input Set : N:\Crf3\RULE60\09966755.raw

Output Set: N:\CRF3\01152002\I966755.raw

1 <110> APPLICANT: Andrew, David P.
2 Zabel, Brian A.
3 Ponath, Paul D.
4 <120> TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
5 IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
6 <130> FILE REFERENCE: LKS98-16
7 <140> CURRENT APPLICATION NUMBER: 09/966,755
8 <141> CURRENT FILING DATE: 2001-09-28
10 <150> PRIOR APPLICATION NUMBER: US/09/266,464
11 <151> PRIOR FILING DATE: 1999-03-11
14 <160> NUMBER OF SEQ ID NOS: 7
15 <170> SOFTWARE: FastSEQ for Windows Version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2577
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (58)...(1131)
24 <400> SEQUENCE: 1

25	aatattttcc ttgacctaat gccatcttgt gtccccttgc agagccctat tctaac atg	60
26		Met
27		1
28	gct gat gac tat ggc tct gaa tcc aca tct tcc atg gaa gac tac gtt	108
29	Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr Val	
30	5 10 15	
31	aac ttc aac ttc act gac ttc tac tgt gag aaa aac aat gtc agg cag	156
32	Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln	
33	20 25 30	
34	ttt gcg agc cat ttc ctc cca ccc ttg tac tgg ctc gtg ttc atc gtg	204
35	Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val	
36	35 40 45	
37	ggt gcc ttg ggc aac agt ctt gtt atc ctt gtc tac tgg tac tgc aca	252
38	Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr	
39	50 55 60 65	
40	aga gtg aag acc atg acc gac atg ttc ctt ttg aat ttg gca att gct	300
41	Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala	
42	70 75 80	
43	gac ctc ctc ttt ctt gtc act ctt ccc ttc tgg gcc att gct gct gct	348
44	Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala	
45	85 90 95	
46	gac cag tgg aag ttc cag acc ttc atg tgc aag gtg gtc aac agc atg	396
47	Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met	
48	100 105 110	
49	tac aag atg aac ttc tac agc tgt gtg ttg ctg atc atg tgc atc agc	444
50	Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser	
51	115 120 125	

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52	gtg gac agg tac att gcc att gcc cag gcc atg aga gca cat act tgg	492
53	Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp	
54	130 135 140 145	
55	agg gag aaa agg ctt ttg tac agc aaa atg gtt tgc ttt acc atc tgg	540
56	Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp	
57	150 155 160	
58	gta ttg gca gct gct ctc tgc atc cca gaa atc tta tac agc caa atc	588
59	Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile	
60	165 170 175	
61	aag gag gaa tcc ggc att gct atc tgc acc atg gtt tac cct agc gat	636
62	Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp	
63	180 185 190	
64	gag agc acc aaa ctg aag tca gct gtc ttg acc ctg aag gtc att ctg	684
65	Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu	
66	195 200 205	
67	ggg ttc ttc ctt ccc ttc gtg gtc atg gct tgc tgc tat acc atc atc	732
68	Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile	
69	210 215 220 225	
70	att cac acc ctg ata caa gcc aag aag tct tcc aag cac aaa gcc cta	780
71	Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu	
72	230 235 240	
73	aaa gtg acc atc act gtc ctg acc gtc ttt gtc ttg tct cag ttt ccc	828
74	Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro	
75	245 250 255	
76	tac aac tgc att ttg ttg gtg cag acc att gac gcc tat gcc atg ttc	876
77	Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe	
78	260 265 270	
79	atc tcc aac tgt gcc gtt tcc acc aac att gac atc tgc ttc cag gtc	924
80	Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val	
81	275 280 285	
82	acc cag acc atc gcc ttc ttc cac agt tgc ctg aac cct gtt ctc tat	972
83	Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr	
84	290 295 300 305	
85	gtt ttt gtg ggt gag aga ttc cgc cgg gat ctc gtg aaa acc ctg aag	1020
86	Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys	
87	310 315 320	
88	aac ttg ggt tgc atc agc cag gcc cag tgg gtt tca ttt aca agg aga	1068
89	Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg	
90	325 330 335	
91	gag gga agc ttg aag ctg tcg tct atg ttg ctg gag aca acc tca gga	1116
92	Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Ser Gly	
93	340 345 350	
94	gca ctc tcc ctc tga ggggtcttct ctgaggtgca tggttctttt ggaagaaatg	1171
95	Ala Leu Ser Leu *	
96	355	
97	agaaatacat gaaacagttt cccactgat gggaccagag agagtgaaag agaaaagaaa	1231
98	actcagaaag ggatgaatct gaactatatg attacttgta gtcagaattt gccaaagcaa	1291
99	atatttcaaa atcaactgac tagtgcagga ggctgttgat tggctcttga ctgtgatgcc	1351
100	cgcaattctc aaaggaggac taaggaccgg cactgtggag caccctggct ttgccactcg	1411

RAW SEQUENCE LISTING

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Input Set : N:\Crif3\RULE60\09966755.raw

Output Set: N:\CRF3\01152002\I966755.raw

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101      ccggagcatc aatgccgctg cctctggagg agcccttgga ttttctccat gcaactgtgaa 1471
102      cttctgtggc ttcagttctc atgctgcctc ttccaaaagg ggacacagaa gcaactggctg 1531
103      ctgctacaga ccgcaaaagc agaaaagtttc gtgaaaatgt ccatcttttg gaaattttct 1591
104      accctgctct tgagcctgat aacccatgcc aggtcttata gattcctgat ctagaacctt 1651
105      tccaggcaat ctgagacctc atttccttct gttctccttg ttctgttctg ggccagtga 1711
106      ggtccttggt ctgattttga aacgatctgc aggtcttgcc agtgaacccc tggacaactg 1771
107      accacaccca caaggcatcc aaagtctggt ggcttccaat ccattttctgt gtctgtctgg 1831
108      aggttttaac ctagacaagg attccgctta ttcttggtta tgggtgacagt gtctctccat 1891
109      ggcctgagca gggagattat aacagctggg ttgcgaggag ccagccttg cctgtgtgta 1951
110      ggcttgttct gttgagtggc acttgctttg ggtccaccgt ctgtctgctc cctagaaaat 2011
111      gggtctggtc ttttgccctt cttctttctg aggccactt tattctgagg aatacagtga 2071
112      gcagatatgg gcagcagcca ggtagggcaa aggggtgaag cgcaggcctt gctggaaggc 2131
113      tatttacttc catgcttctc cttttcttac tctatagtgg caacatttta aaagctttta 2191
114      acttagagat taggctgaaa aaaataagta atggaattca cctttgcac tttgtgtct 2251
115      ttcttatcat gatttggaac aatgcatcac ctttgaaaat atttcacata ttggaaaagt 2311
116      gctttttaat gtgtatatga agcattaatt acttgctact ttctttacce tgtctcaata 2371
117      ttttaagtgt gtgcaattaa agatcaaata gatacattaa gagtgtgaag gctgggtctga 2431
118      aggtagttag ctatctcaat cggattgttc aactcagtt acagattgaa ctcttgttc 2491
119      tacttccctg cttctctcta ctgcaattga ctagtcttta aaaaaaagtg tgaagagtaa 2551
120      gcaataggga taaggaaata agatct
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123 <211> LENGTH: 357
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 2
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129      Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg
130      20          25          30
131      Gln Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile
132      35          40          45
133      Val Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys
134      50          55          60
135      Thr Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile
136      65          70          75          80
137      Ala Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala
138      85          90          95
139      Ala Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser
140      100         105         110
141      Met Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile
142      115         120         125
143      Ser Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr
144      130         135         140
145      Trp Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile
146      145         150         155         160
147      Trp Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln
148      165         170         175
149      Ile Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser
150      180         185         190

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151    Asp Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile
152              195                200                205
153    Leu Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile
154              210                215                220
155    Ile Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala
156              225                230                235                240
157    Leu Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe
158              245                250                255
159    Pro Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met
160              260                265                270
161    Phe Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln
162              275                280                285
163    Val Thr Gln Thr Ile Ala Phe His Ser Cys Leu Asn Pro Val Leu
164              290                295                300
165    Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
166              305                310                315                320
167    Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
168              325                330                335
169    Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
170              340                345                350
171    Gly Ala Leu Ser Leu
172              355

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174 <210> SEQ ID NO: 3

175 <211> LENGTH: 26

176 <212> TYPE: PRT

177 <213> ORGANISM: Artificial Sequence

178 <220> FEATURE:

179 <223> OTHER INFORMATION: NH2-Terminal Peptide of Human GPR-9-6

180 <400> SEQUENCE: 3

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181    Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
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183    Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys
184      20          25

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186 <210> SEQ ID NO: 4

187 <211> LENGTH: 35

188 <212> TYPE: DNA

189 <213> ORGANISM: Artificial Sequence

190 <220> FEATURE:

191 <223> OTHER INFORMATION: Oligonucleotide primer

192 <400> SEQUENCE: 4

193 tcgaagggat ccctaacatg gctgatgact atggc

35

195 <210> SEQ ID NO: 5

196 <211> LENGTH: 35

197 <212> TYPE: DNA

198 <213> ORGANISM: Artificial Sequence

199 <220> FEATURE:

200 <223> OTHER INFORMATION: Oligonucleotide primer

201 <400> SEQUENCE: 5

202 aagaagtcta gaaccctca gagggagagt gctcc

35

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204 <210> SEQ ID NO: 6
205 <211> LENGTH: 30
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Oligonucleotide primer
210 <400> SEQUENCE: 6
211      tcgaagaagc ttatgaacct gtggctcctg
213 <210> SEQ ID NO: 7
214 <211> LENGTH: 30
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Oligonucleotide primer
219 <400> SEQUENCE: 7
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